Serial Number: 08/977,862

CRF Processing Date: 1/16/98
Edited by: _____
Verified by: _____ (STIC staff)

☐ Changed a file from non-ASCII to ASCII

☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.

☐ Edited a format error in the Current Application Data section, specifically: _____

☐ Edited the Current Application Data section with the actual current number. The number imported by the applicant was ☐ the prior application data; or ☐ other _____.

☐ Added the mandatory heading and subheadings for "Current Application Data".

☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____

☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____

☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____

☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐ Inserted colons after headings/subheadings. Headings edited included: _____

☐ Deleted extra, invalid, headings used by an applicant, specifically: _____

☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as_____ .

☐ Inserted mandatory headings, specifically: _____

☐ Corrected an obvious error in the response, specifically: _____

☐ Edited identifiers where upper case is used but lower case is required, or vice versa.

☐ Corrected an error in the Number of Sequences field, specifically: _____

☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

☑ Other: _deleted stray mark under (vii) PRIOR APP. DATA' section_
_____
_____
_____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

1815

INPUT SET: S22663.raw

> This Raw Listing contains the General Information Section and up to the first 5 pages.

ENTERED

```
 1                              SEQUENCE LISTING
 2
 3    (1)    General Information
 4
 5           (i) APPLICANT: Lawrence, Geoffrey
 6
 7           (ii) TITLE OF THE INVENTION: Novel Compounds
 8
 9
10           (iii) NUMBER OF SEQUENCES: 6
11
12           (iv) CORRESPONDENCE ADDRESS:
13              (A) ADDRESSEE: Ratner & Prestia
14              (B) STREET: P.O. Box 980
15              (C) CITY: Valley Forge
16              (D) STATE: PA
17              (E) COUNTRY: USA
18              (F) ZIP: 19482
19
20           (v) COMPUTER READABLE FORM:
21              (A) MEDIUM TYPE: Diskette
22              (B) COMPUTER: IBM Compatible
23              (C) OPERATING SYSTEM: DOS
24              (D) SOFTWARE: FastSEQ for Windows Version 2.0
25
26           (vi) CURRENT APPLICATION DATA:
27              (A) APPLICATION NUMBER:To be assigned
28              (B) FILING DATE: Herewith
29              (C) CLASSIFICATION:
30
31           (vii) PRIOR APPLICATION DATA:
32              (A) APPLICATION NUMBER: GB 96 24677.2
33              (B) FILING DATE: Filed November 27, 1996
34
35
36              (A) APPLICATION NUMBER: GB 9709463.5
37              (B) FILING DATE: May 9, 1997
38
39           (viii) ATTORNEY/AGENT INFORMATION:
40              (A) NAME: Prestia, Paul F.
41              (B) REGISTRATION NUMBER: 23,031
42              (C) REFERENCE/DOCKET NUMBER:  GH30170
43
44           (ix) TELECOMMUNICATION INFORMATION:
45              (A) TELEPHONE: 610-407-0700
46              (B) TELEFAX: 610-407-0701
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--> OK 27

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47              (C) TELEX: 846169
48
49
50          (2) INFORMATION FOR SEQ ID NO:1:
51
52      (i) SEQUENCE CHARACTERISTICS:
53          (A) LENGTH: 1200 base pairs
54          (B) TYPE: nucleic acid
55          (C) STRANDEDNESS: single
56          (D) TOPOLOGY: linear
57
58      (ii) MOLECULE TYPE: cDNA
59
60      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
61
62  ATGGTGCGCC CCCTGAACCC GCGACCGCTG CCGCCCGTAG TCCTGATGTT GCTGCTGCTG        60
63  CTGCCGCCGT CGCCGCTGCC TCTCGCAGCC GGAGACCCCC TTCCCACAGA AAGCCGACTC       120
64  ATGAACAGCT GTCTCCAGGC CAGGAGGAAG TGCCAGGCTG ATCCCACCTG CAGTGCTGCC       180
65  TACCACCACC TGGATTCCTG CACCTCTAGC ATAAGCACCC CACTGCCCTC AGAGGAGCCT       240
66  TCGGTCCCTG CTGACTGCCT GGAGGCAGCA CAGCAACTCA GGAACAGCTC TCTGATAGGC       300
67  TGCATGTGCC ACCGGCGCAT GAAGAACCAG GTTGCCTGCT TGGACATCTA TTGGACCGTT       360
68  CACCGTGCCC GCAGCCTTGG TAACTATGAG CTGGATGTCT CCCCCTATGA AGACACAGTG       420
69  ACCAGCAAAC CCTGGAAAAT GAATCTCAGC AAACTGAACA TGCTCAAACC AGACTCAGAC       480
70  CTCTGCCTCA AGTTTGCCAT GCTGTGTACT CTCAATGACA AGTGTGACCG GCTGCGCAAG       540
71  GCCTACGGGG AGGCGTGCTC CGGGCCCCAC TGCCAGCGCC ACGTCTGCCT CAGGCAGCTG       600
72  CTCACTTTCT TCGAGAAGGC CGCCGAGCCC CACGCGCAGG GCCTGCTACT GTGCCCATGT       660
73  GCCCCCAACG ACCGGGGCTG CGGGGAGCGC CGGCGCAACA CCATCGCCCC CAACTGCGCG       720
74  CTGCCGCCTG TGGCCCCCAA CTGCCTGGAG CTGCGGCGCC TCTGCTTCTC CGACCCGCTT       780
75  TGCAGATCAC GCCTGGTGGA TTTCCAGACC CACTGCCATC CCATGGACAT CCTAGGAACT       840
76  TGTGCAACAG AGCAGTCCAG ATGTCTACGA GCATACCTGG GGCTGATTGG GACTGCCATG       900
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78  AGTGGCAACC TGCAGGAGGA GTGTGAAATG CTGGAAGGGT CTTCTCCCA CAACCCCTGC      1020
79  CTCACGGAGG CCATTGCAGC TAAGATGCGT TTTCACAGCC AACTCTTCTC CCAGGACTGG      1080
80  CCACACCCTA CCTTTGCTGT GATGGCACAC CAGAATGAAA ACCCTGCTGT GAGGCCACAG      1140
81  CCCTGGGTGC CCTCTCTTTT CTCCTGCACG CTTCCCTTGA TTCTGCTCCT GAGCCTATGG      1200
82
83          (2) INFORMATION FOR SEQ ID NO:2:
84
85      (i) SEQUENCE CHARACTERISTICS:
86          (A) LENGTH: 400 amino acids
87          (B) TYPE: amino acid
88          (C) STRANDEDNESS: single
89          (D) TOPOLOGY: linear
90
91      (ii) MOLECULE TYPE: peptide
92
93      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
94
95  Met Val Arg Pro Leu Asn Pro Arg Pro Leu Pro Pro Val Val Leu Met
96   1               5                  10                  15
97  Leu Leu Leu Leu Leu Pro Pro Ser Pro Leu Pro Leu Ala Ala Gly Asp
98              20                  25                  30
99  Pro Leu Pro Thr Glu Ser Arg Leu Met Asn Ser Cys Leu Gln Ala Arg
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INPUT SET: S22663.raw

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102          50                    55                    60
103      Asp Ser Cys Thr Ser Ser Ile Ser Thr Pro Leu Pro Ser Glu Glu Pro
104      65                    70                    75                    80
105      Ser Val Pro Ala Asp Cys Leu Glu Ala Ala Gln Gln Leu Arg Asn Ser
106                85                    90                    95
107      Ser Leu Ile Gly Cys Met Cys His Arg Arg Met Lys Asn Gln Val Ala
108               100                   105                   110
109      Cys Leu Asp Ile Tyr Trp Thr Val His Arg Ala Arg Ser Leu Gly Asn
110               115                   120                   125
111      Tyr Glu Leu Asp Val Ser Pro Tyr Glu Asp Thr Val Thr Ser Lys Pro
112          130                   135                   140
113      Trp Lys Met Asn Leu Ser Lys Leu Asn Met Leu Lys Pro Asp Ser Asp
114      145                   150                   155                   160
115      Leu Cys Leu Lys Phe Ala Met Leu Cys Thr Leu Asn Asp Lys Cys Asp
116               165                   170                   175
117      Arg Leu Arg Lys Ala Tyr Gly Glu Ala Cys Ser Gly Pro His Cys Gln
118               180                   185                   190
119      Arg His Val Cys Leu Arg Gln Leu Leu Thr Phe Phe Glu Lys Ala Ala
120          195                   200                   205
121      Glu Pro His Ala Gln Gly Leu Leu Leu Cys Pro Cys Ala Pro Asn Asp
122          210                   215                   220
123      Arg Gly Cys Gly Glu Arg Arg Arg Asn Thr Ile Ala Pro Asn Cys Ala
124      225                   230                   235                   240
125      Leu Pro Pro Val Ala Pro Asn Cys Leu Glu Leu Arg Arg Leu Cys Phe
126               245                   250                   255
127      Ser Asp Pro Leu Cys Arg Ser Arg Leu Val Asp Phe Gln Thr His Cys
128               260                   265                   270
129      His Pro Met Asp Ile Leu Gly Thr Cys Ala Thr Glu Gln Ser Arg Cys
130               275                   280                   285
131      Leu Arg Ala Tyr Leu Gly Leu Ile Gly Thr Ala Met Thr Pro Asn Phe
132          290                   295                   300
133      Val Ser Asn Val Asn Thr Ser Val Ala Leu Ser Cys Thr Cys Arg Gly
134      305                   310                   315                   320
135      Ser Gly Asn Leu Gln Glu Glu Cys Glu Met Leu Glu Gly Phe Phe Ser
136               325                   330                   335
137      His Asn Pro Cys Leu Thr Glu Ala Ile Ala Ala Lys Met Arg Phe His
138               340                   345                   350
139      Ser Gln Leu Phe Ser Gln Asp Trp Pro His Pro Thr Phe Ala Val Met
140          355                   360                   365
141      Ala His Gln Asn Glu Asn Pro Ala Val Arg Pro Gln Pro Trp Val Pro
142          370                   375                   380
143      Ser Leu Phe Ser Cys Thr Leu Pro Leu Ile Leu Leu Leu Ser Leu Trp
144      385                   390                   395                   400
145
146              (2) INFORMATION FOR SEQ ID NO:3:
147
148          (i) SEQUENCE CHARACTERISTICS:
149              (A) LENGTH: 1200 base pairs
150              (B) TYPE: nucleic acid
151              (C) STRANDEDNESS: single
152              (D) TOPOLOGY: linear
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PAGE: 4

RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/977,862*

DATE: 01/21/98
TIME: 09:56:20

INPUT SET: S22663.raw

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154        (ii) MOLECULE TYPE: cDNA
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156        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
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159    CTGCCGCCGT CGCCGCTGCC TCTCGCAGCC GGAGACCCCC TTCCCACAGA AAGCCGACTC     120
160    ATGAACAGCT GTCTCCAGGC CAGGAGGAAG TGCCAGGCTG ATCCCACCTG CAGTGATGCC     180
161    TACCACCACC TGGATTCCTG CACCTCTAGC ATAAGCACCC CACTGCCCTC AGAGGAGCCT     240
162    TCGGTCCCTG CTGACTGCCT GGAGGCAGCA CAGCAACTCA GGAACAGCTC TCTGATAGGC     300
163    TGCATGTGCC ACCGGCGCAT GAAGAACCAG GTTGCCTGCT TGGACATCTA TTGGACCGTT     360
164    CACCGTGCCC GCAGCCTTGG TAACTATGAG CTGGATGTCT CCCCCTATGA AGACACAGTG     420
165    ACCAGCAAAC CCTGGAAAAT GAATCTCAGC AAACTGAACA TGCTCAAACC AGACTCAGAC     480
166    CTCTGCCTCA AGTTTGCCAT GCTGTGTACT CTCAATGACA AGTGTGACCG GCTGCGCAAG     540
167    GCCTACGGGG AGGCGTGCTC CGGGCCCCAC TGCCAGCGCC ACGTCTGCCT CAGGCAGCTG     600
168    CTCACTTTCT TCGAGAAGGC CGCCGAGCCC CACGCGCAGG GCCTGCTACT GTGCCCATGT     660
169    GCCCCCAACG ACCGGGGCTG CGGGGAGCGC CGGCGCAACA CCATCGCCCC CAACTGCGCG     720
170    CTGCCGCCTG TGGCCCCCAA CTGCCTGGAG CTGCGGCGCC TCTGCTTCTC CGACCCGCTT     780
171    TGCAGATCAC GCCTGGTGGA TTTCCAGACC CACTGCCATC CCATGGACAT CCTAGGAACT     840
172    TGTGCAACAG AGCAGTCCAG ATGTCTACGA GCATACCTGG GGCTGATTGG GACTGCCATG     900
173    ACCCCCAACT TTGTCAGCAA TGTCAACACC AGTGTTGCCT TAAGCTGCAC CTGCCGAGGC     960
174    AGTGGCAACC TGCAGGAGGA GTGTGAAATG CTGGAAGGGT CTTCTCCCA CAACCCCTGC    1020
175    CTCACGGAGG CCATTGCAGC TAAGATGCGT TTTCACAGCC AACTCTTCTC CCAGGACTGG    1080
176    CCACACCCTA CCTTTGCTGT GATGGCACAC CAGAATGAAA ACCCTGCTGT GAGGCCACAG    1140
177    CCCTGGGTGC CCTCTCTTTT CTCCTGCACG CTTCCCTTGA TTCTGCTCCT GAGCCTATGG    1200
178
179        (2) INFORMATION FOR SEQ ID NO:4:
180
181        (i) SEQUENCE CHARACTERISTICS:
182            (A) LENGTH: 400 amino acids
183            (B) TYPE: amino acid
184            (C) STRANDEDNESS: single
185            (D) TOPOLOGY: linear
186
187        (ii) MOLECULE TYPE: peptide
188
189        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
190
191    Met Val Arg Pro Leu Asn Pro Arg Pro Leu Pro Pro Val Val Leu Met
192    1               5                   10                  15
193    Leu Leu Leu Leu Leu Pro Pro Ser Pro Leu Pro Leu Ala Ala Gly Asp
194                    20                  25                  30
195    Pro Leu Pro Thr Glu Ser Arg Leu Met Asn Ser Cys Leu Gln Ala Arg
196                35                  40                  45
197    Arg Lys Cys Gln Ala Asp Pro Thr Cys Ser Asp Ala Tyr His His Leu
198        50                  55                  60
199    Asp Ser Cys Thr Ser Ser Ile Ser Thr Pro Leu Pro Ser Glu Glu Pro
200    65                  70                  75                  80
201    Ser Val Pro Ala Asp Cys Leu Glu Ala Ala Gln Gln Leu Arg Asn Ser
202                    85                  90                  95
203    Ser Leu Ile Gly Cys Met Cys His Arg Arg Met Lys Asn Gln Val Ala
204                    100                 105                 110
205    Cys Leu Asp Ile Tyr Trp Thr Val His Arg Ala Arg Ser Leu Gly Asn
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INPUT SET: S22663.raw

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207    Tyr Glu Leu Asp Val Ser Pro Tyr Glu Asp Thr Val Thr Ser Lys Pro
208          130                      135                      140
209    Trp Lys Met Asn Leu Ser Lys Leu Asn Met Leu Lys Pro Asp Ser Asp
210    145                      150                      155                      160
211    Leu Cys Leu Lys Phe Ala Met Leu Cys Thr Leu Asn Asp Lys Cys Asp
212              165                      170                      175
213    Arg Leu Arg Lys Ala Tyr Gly Glu Ala Cys Ser Gly Pro His Cys Gln
214              180                      185                      190
215    Arg His Val Cys Leu Arg Gln Leu Leu Thr Phe Phe Glu Lys Ala Ala
216          195                      200                      205
217    Glu Pro His Ala Gln Gly Leu Leu Leu Cys Pro Cys Ala Pro Asn Asp
218          210                      215                      220
219    Arg Gly Cys Gly Glu Arg Arg Arg Asn Thr Ile Ala Pro Asn Cys Ala
220    225                      230                      235                      240
221    Leu Pro Pro Val Ala Pro Asn Cys Leu Glu Leu Arg Arg Leu Cys Phe
222              245                      250                      255
223    Ser Asp Pro Leu Cys Arg Ser Arg Leu Val Asp Phe Gln Thr His Cys
224              260                      265                      270
225    His Pro Met Asp Ile Leu Gly Thr Cys Ala Thr Glu Gln Ser Arg Cys
226          275                      280                      285
227    Leu Arg Ala Tyr Leu Gly Leu Ile Gly Thr Ala Met Thr Pro Asn Phe
228          290                      295                      300
229    Val Ser Asn Val Asn Thr Ser Val Ala Leu Ser Cys Thr Cys Arg Gly
230    305                      310                      315                      320
231    Ser Gly Asn Leu Gln Glu Glu Cys Glu Met Leu Glu Gly Phe Phe Ser
232              325                      330                      335
233    His Asn Pro Cys Leu Thr Glu Ala Ile Ala Ala Lys Met Arg Phe His
234          . 340                      345                      350
235    Ser Gln Leu Phe Ser Gln Asp Trp Pro His Pro Thr Phe Ala Val Met
236          355                      360                      365
237    Ala His Gln Asn Glu Asn Pro Ala Val Arg Pro Gln Pro Trp Val Pro
238          370                      375                      380
239    Ser Leu Phe Ser Cys Thr Leu Pro Leu Ile Leu Leu Leu Ser Leu Trp
240    385                      390                      395                      400
241
242              (2) INFORMATION FOR SEQ ID NO:5:
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244          (i) SEQUENCE CHARACTERISTICS:
245              (A) LENGTH: 519 base pairs
246              (B) TYPE: nucleic acid
247              (C) STRANDEDNESS: single
248              (D) TOPOLOGY: linear
249
250          (ii) MOLECULE TYPE: cDNA
251
252          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
253
254    GAGCGCCGGC GCAACACCAT CGCCCCCAAC TGCGCGCTGC CGCCTGTGGC CCCCAACTGC        60
255    CTGGAGCTGC GGCGCCTCTG CTTCTCCGAC CCGCTTTGCA GATCACGCCT GGTGGATTTC       120
256    CAGACCCACT GCCATCCCAT GGACATCCTA GGAACTTGTG CAACAGAGCA GTCCAGATGT       180
257    CTACGAGCAT ACCTGGGGCT GATTGGGACT GCCATGACCC CCAACTTTGT CAGCAATGTC       240
258    AACACCAGTG TTGCCTTAAG CTGCACCTGC CGAGGCAGTG GCAACCTGCA GGAGGAGTGT       300
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION   *US/08/977,862*

INPUT SET: S22663.raw

Line	Error	Original Text
27	Wrong application Serial Number	(A) APPLICATION NUMBER:To be assigned

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/977,862*

DATE: 01/16/98
TIME: 14:03:57

INPUT SET: S22663.raw

1815

This Raw Listing contains the General
Information Section and up to the first 5 pages.

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 1                              SEQUENCE LISTING
 2
 3    (1)     General Information
 4
 5            (i) APPLICANT: Lawrence, Geoffrey
 6
 7            (ii) TITLE OF THE INVENTION: Novel Compounds
 8
 9
10            (iii) NUMBER OF SEQUENCES: 6
11
12            (iv) CORRESPONDENCE ADDRESS:
13              (A) ADDRESSEE: Ratner & Prestia
14              (B) STREET: P.O. Box 980
15              (C) CITY: Valley Forge
16              (D) STATE: PA
17              (E) COUNTRY: USA
18              (F) ZIP: 19482
19
20            (v) COMPUTER READABLE FORM:
21              (A) MEDIUM TYPE: Diskette
22              (B) COMPUTER: IBM Compatible
23              (C) OPERATING SYSTEM: DOS
24              (D) SOFTWARE: FastSEQ for Windows Version 2.0
25
26            (vi) CURRENT APPLICATION DATA:
27              (A) APPLICATION NUMBER:To be assigned
28              (B) FILING DATE: Herewith
29              (C) CLASSIFICATION:
30
31            (vii) PRIOR APPLICATION DATA:
32              (A) APPLICATION NUMBER: GB 96 24677.2
33              (B) FILING DATE: Filed November 27, 1996
34
35              (A) APPLICATION NUMBER: GB 9709463.5
36              (B) FILING DATE: May 9, 1997
37
38            (viii) ATTORNEY/AGENT INFORMATION:
39              (A) NAME: Prestia, Paul F.
40              (B) REGISTRATION NUMBER: 23,031
41              (C) REFERENCE/DOCKET NUMBER:  GH30170
42
43            (ix) TELECOMMUNICATION INFORMATION:
44              (A) TELEPHONE: 610-407-0700
45              (B) TELEFAX: 610-407-0701
46              (C) TELEX: 846169
```

```
47
48
49            (2) INFORMATION FOR SEQ ID NO:1:
50
51        (i) SEQUENCE CHARACTERISTICS:
52           (A) LENGTH: 1200 base pairs
53           (B) TYPE: nucleic acid
54           (C) STRANDEDNESS: single
55           (D) TOPOLOGY: linear
56
57        (ii) MOLECULE TYPE: cDNA
58
59        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
60
61    ATGGTGCGCC CCCTGAACCC GCGACCGCTG CCGCCCGTAG TCCTGATGTT GCTGCTGCTG      60
62    CTGCCGCCGT CGCCGCTGCC TCTCGCAGCC GGAGACCCCC TTCCCACAGA AAGCCGACTC     120
63    ATGAACAGCT GTCTCCAGGC CAGGAGGAAG TGCCAGGCTG ATCCCACCTG CAGTGCTGCC     180
64    TACCACCACC TGGATTCCTG CACCTCTAGC ATAAGCACCC CACTGCCCTC AGAGGAGCCT     240
65    TCGGTCCCTG CTGACTGCCT GGAGGCAGCA CAGCAACTCA GGAACAGCTC TCTGATAGGC     300
66    TGCATGTGCC ACCGGCGCAT GAAGAACCAG GTTGCCTGCT TGGACATCTA TTGGACCGTT     360
67    CACCGTGCCC GCAGCCTTGG TAACTATGAG CTGGATGTCT CCCCCTATGA AGACACAGTG     420
68    ACCAGCAAAC CCTGGAAAAT GAATCTCAGC AAACTGAACA TGCTCAAACC AGACTCAGAC     480
69    CTCTGCCTCA AGTTTGCCAT GCTGTGTACT CTCAATGACA AGTGTGACCG GCTGCGCAAG     540
70    GCCTACGGGG AGGCGTGCTC CGGGCCCCAC TGCCAGCGCC ACGTCTGCCT CAGGCAGCTG     600
71    CTCACTTTCT TCGAGAAGGC CGCCGAGCCC CACGCGCAGG GCCTGCTACT GTGCCCATGT     660
72    GCCCCCAACG ACCGGGGCTG CGGGGAGCGC CGGCGCAACA CCATCGCCCC CAACTGCGCG     720
73    CTGCCGCCTG TGGCCCCCAA CTGCCTGGAG CTGCGGCGCC TCTGCTTCTC CGACCCGCTT     780
74    TGCAGATCAC GCCTGGTGGA TTTCCAGACC CACTGCCATC CCATGGACAT CCTAGGAACT     840
75    TGTGCAACAG AGCAGTCCAG ATGTCTACGA GCATACCTGG GGCTGATTGG GACTGCCATG     900
76    ACCCCCAACT TTGTCAGCAA TGTCAACACC AGTGTTGCCT TAAGCTGCAC CTGCCGAGGC     960
77    AGTGGCAACC TGCAGGAGGA GTGTGAAATG CTGGAAGGGT TCTTCTCCCA CAACCCCTGC    1020
78    CTCACGGAGG CCATTGCAGC TAAGATGCGT TTTCACAGCC AACTCTTCTC CCAGGACTGG    1080
79    CCACACCCTA CCTTTGCTGT GATGGCACAC CAGAATGAAA ACCCTGCTGT GAGGCCACAG    1140
80    CCCTGGGTGC CCTCTCTTTT CTCCTGCACG CTTCCCTTGA TTCTGCTCCT GAGCCTATGG    1200
81
82            (2) INFORMATION FOR SEQ ID NO:2:
83
84        (i) SEQUENCE CHARACTERISTICS:
85           (A) LENGTH: 400 amino acids
86           (B) TYPE: amino acid
87           (C) STRANDEDNESS: single
88           (D) TOPOLOGY: linear
89
90        (ii) MOLECULE TYPE: peptide
91
92        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
93
94    Met Val Arg Pro Leu Asn Pro Arg Pro Leu Pro Pro Val Val Leu Met
95     1               5                  10                  15
96    Leu Leu Leu Leu Leu Pro Pro Ser Pro Leu Pro Leu Ala Ala Gly Asp
97                  20                  25                  30
98    Pro Leu Pro Thr Glu Ser Arg Leu Met Asn Ser Cys Leu Gln Ala Arg
99                  35                  40                  45
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RAW SEQUENCE LISTING
PATENT APPLICATION   *US/08/977,862*

INPUT SET: S22663.raw

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102    Asp Ser Cys Thr Ser Ser Ile Ser Thr Pro Leu Pro Ser Glu Glu Pro
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104    Ser Val Pro Ala Asp Cys Leu Glu Ala Ala Gln Gln Leu Arg Asn Ser
105                85              90              95
106    Ser Leu Ile Gly Cys Met Cys His Arg Arg Met Lys Asn Gln Val Ala
107            100             105             110
108    Cys Leu Asp Ile Tyr Trp Thr Val His Arg Ala Arg Ser Leu Gly Asn
109        115             120             125
110    Tyr Glu Leu Asp Val Ser Pro Tyr Glu Asp Thr Val Thr Ser Lys Pro
111        130             135             140
112    Trp Lys Met Asn Leu Ser Lys Leu Asn Met Leu Lys Pro Asp Ser Asp
113    145             150             155             160
114    Leu Cys Leu Lys Phe Ala Met Leu Cys Thr Leu Asn Asp Lys Cys Asp
115                165             170             175
116    Arg Leu Arg Lys Ala Tyr Gly Glu Ala Cys Ser Gly Pro His Cys Gln
117            180             185             190
118    Arg His Val Cys Leu Arg Gln Leu Leu Thr Phe Phe Glu Lys Ala Ala
119        195             200             205
120    Glu Pro His Ala Gln Gly Leu Leu Leu Cys Pro Cys Ala Pro Asn Asp
121        210             215             220
122    Arg Gly Cys Gly Glu Arg Arg Arg Asn Thr Ile Ala Pro Asn Cys Ala
123    225             230             235             240
124    Leu Pro Pro Val Ala Pro Asn Cys Leu Glu Leu Arg Arg Leu Cys Phe
125                245             250             255
126    Ser Asp Pro Leu Cys Arg Ser Arg Leu Val Asp Phe Gln Thr His Cys
127            260             265             270
128    His Pro Met Asp Ile Leu Gly Thr Cys Ala Thr Glu Gln Ser Arg Cys
129        275             280             285
130    Leu Arg Ala Tyr Leu Gly Leu Ile Gly Thr Ala Met Thr Pro Asn Phe
131        290             295             300
132    Val Ser Asn Val Asn Thr Ser Val Ala Leu Ser Cys Thr Cys Arg Gly
133    305             310             315             320
134    Ser Gly Asn Leu Gln Glu Glu Cys Glu Met Leu Glu Gly Phe Phe Ser
135                325             330             335
136    His Asn Pro Cys Leu Thr Glu Ala Ile Ala Ala Lys Met Arg Phe His
137            340             345             350
138    Ser Gln Leu Phe Ser Gln Asp Trp Pro His Pro Thr Phe Ala Val Met
139        355             360             365
140    Ala His Gln Asn Glu Asn Pro Ala Val Arg Pro Gln Pro Trp Val Pro
141    370             375             380
142    Ser Leu Phe Ser Cys Thr Leu Pro Leu Ile Leu Leu Leu Ser Leu Trp
143    385             390             395             400
144
145            (2) INFORMATION FOR SEQ ID NO:3:
146
147        (i) SEQUENCE CHARACTERISTICS:
148            (A) LENGTH: 1200 base pairs
149            (B) TYPE: nucleic acid
150            (C) STRANDEDNESS: single
151            (D) TOPOLOGY: linear
152
```

```
153              (ii) MOLECULE TYPE: cDNA
154
155              (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
156
157    ATGGTGCGCC CCCTGAACCC GCGACCGCTG CCGCCCGTAG TCCTGATGTT GCTGCTGCTG      60
158    CTGCCGCCGT CGCCGCTGCC TCTCGCAGCC GGAGACCCCC TTCCCACAGA AAGCCGACTC     120
159    ATGAACAGCT GTCTCCAGGC CAGGAGGAAG TGCCAGGCTG ATCCCACCTG CAGTGATGCC     180
160    TACCACCACC TGGATTCCTG CACCTCTAGC ATAAGCACCC CACTGCCCTC AGAGGAGCCT     240
161    TCGGTCCCTG CTGACTGCCT GGAGGCAGCA CAGCAACTCA GGAACAGCTC TCTGATAGGC     300
162    TGCATGTGCC ACCGGCGCAT GAAGAACCAG GTTGCCTGCT TGGACATCTA TTGGACCGTT     360
163    CACCGTGCCC GCAGCCTTGG TAACTATGAG CTGGATGTCT CCCCCTATGA AGACACAGTG     420
164    ACCAGCAAAC CCTGGAAAAT GAATCTCAGC AAACTGAACA TGCTCAAACC AGACTCAGAC     480
165    CTCTGCCTCA AGTTTGCCAT GCTGTGTACT CTCAATGACA AGTGTGACCG GCTGCGCAAG     540
166    GCCTACGGGG AGGCGTGCTC CGGGCCCCAC TGCCAGCGCC ACGTCTGCCT CAGGCAGCTG     600
167    CTCACTTTCT TCGAGAAGGC CGCCGAGCCC CACGCGCAGG GCCTGCTACT GTGCCCATGT     660
168    GCCCCCAACG ACCGGGGCTG CGGGGAGCGC CGGCGCAACA CCATCGCCCC CAACTGCGCG     720
169    CTGCCGCCTG TGGCCCCCAA CTGCCTGGAG CTGCGGCGCC TCTGCTTCTC CGACCCGCTT     780
170    TGCAGATCAC GCCTGGTGGA TTTCCAGACC CACTGCCATC CCATGGACAT CCTAGGAACT     840
171    TGTGCAACAG AGCAGTCCAG ATGTCTACGA GCATACCTGG GGCTGATTGG GACTGCCATG     900
172    ACCCCCAACT TTGTCAGCAA TGTCAACACC AGTGTTGCCT TAAGCTGCAC CTGCCGAGGC     960
173    AGTGGCAACC TGCAGGAGGA GTGTGAAATG CTGGAAGGGT TCTTCTCCCA CAACCCCTGC    1020
174    CTCACGGAGG CCATTGCAGC TAAGATGCGT TTTCACAGCC AACTCTTCTC CCAGGACTGG    1080
175    CCACACCCTA CCTTTGCTGT GATGGCACAC CAGAATGAAA ACCCTGCTGT GAGGCCACAG    1140
176    CCCTGGGTGC CCTCTCTTTT CTCCTGCACG CTTCCCTTGA TTCTGCTCCT GAGCCTATGG    1200
177
178              (2) INFORMATION FOR SEQ ID NO:4:
179
180          (i) SEQUENCE CHARACTERISTICS:
181             (A) LENGTH: 400 amino acids
182             (B) TYPE: amino acid
183             (C) STRANDEDNESS: single
184             (D) TOPOLOGY: linear
185
186          (ii) MOLECULE TYPE: peptide
187
188          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
189
190    Met Val Arg Pro Leu Asn Pro Arg Pro Leu Pro Pro Val Val Leu Met
191     1               5                  10                  15
192    Leu Leu Leu Leu Leu Pro Pro Ser Pro Leu Pro Leu Ala Ala Gly Asp
193                   20                  25                  30
194    Pro Leu Pro Thr Glu Ser Arg Leu Met Asn Ser Cys Leu Gln Ala Arg
195                   35                  40                  45
196    Arg Lys Cys Gln Ala Asp Pro Thr Cys Ser Asp Ala Tyr His His Leu
197         50                  55                  60
198    Asp Ser Cys Thr Ser Ser Ile Ser Thr Pro Leu Pro Ser Glu Glu Pro
199    65                  70                  75                  80
200    Ser Val Pro Ala Asp Cys Leu Glu Ala Ala Gln Gln Leu Arg Asn Ser
201                   85                  90                  95
202    Ser Leu Ile Gly Cys Met Cys His Arg Arg Met Lys Asn Gln Val Ala
203                  100                 105                 110
204    Cys Leu Asp Ile Tyr Trp Thr Val His Arg Ala Arg Ser Leu Gly Asn
205                  115                 120                 125
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INPUT SET: S22663.raw

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206    Tyr Glu Leu Asp Val Ser Pro Tyr Glu Asp Thr Val Thr Ser Lys Pro
207        130             135             140
208    Trp Lys Met Asn Leu Ser Lys Leu Asn Met Leu Lys Pro Asp Ser Asp
209    145             150             155             160
210    Leu Cys Leu Lys Phe Ala Met Leu Cys Thr Leu Asn Asp Lys Cys Asp
211            165             170             175
212    Arg Leu Arg Lys Ala Tyr Gly Glu Ala Cys Ser Gly Pro His Cys Gln
213            180             185             190
214    Arg His Val Cys Leu Arg Gln Leu Leu Thr Phe Phe Glu Lys Ala Ala
215            195             200             205
216    Glu Pro His Ala Gln Gly Leu Leu Leu Cys Pro Cys Ala Pro Asn Asp
217        210             215             220
218    Arg Gly Cys Gly Glu Arg Arg Arg Asn Thr Ile Ala Pro Asn Cys Ala
219    225             230             235             240
220    Leu Pro Pro Val Ala Pro Asn Cys Leu Glu Leu Arg Arg Leu Cys Phe
221            245             250             255
222    Ser Asp Pro Leu Cys Arg Ser Arg Leu Val Asp Phe Gln Thr His Cys
223            260             265             270
224    His Pro Met Asp Ile Leu Gly Thr Cys Ala Thr Glu Gln Ser Arg Cys
225            275             280             285
226    Leu Arg Ala Tyr Leu Gly Leu Ile Gly Thr Ala Met Thr Pro Asn Phe
227        290             295             300
228    Val Ser Asn Val Asn Thr Ser Val Ala Leu Ser Cys Thr Cys Arg Gly
229    305             310             315             320
230    Ser Gly Asn Leu Gln Glu Glu Cys Glu Met Leu Glu Gly Phe Phe Ser
231            325             330             335
232    His Asn Pro Cys Leu Thr Glu Ala Ile Ala Ala Lys Met Arg Phe His
233            340             345             350
234    Ser Gln Leu Phe Ser Gln Asp Trp Pro His Pro Thr Phe Ala Val Met
235        355             360             365
236    Ala His Gln Asn Glu Asn Pro Ala Val Arg Pro Gln Pro Trp Val Pro
237        370             375             380
238    Ser Leu Phe Ser Cys Thr Leu Pro Leu Ile Leu Leu Leu Ser Leu Trp
239    385             390             395             400
240
241            (2) INFORMATION FOR SEQ ID NO:5:
242
243            (i) SEQUENCE CHARACTERISTICS:
244                (A) LENGTH: 519 base pairs
245                (B) TYPE: nucleic acid
246                (C) STRANDEDNESS: single
247                (D) TOPOLOGY: linear
248
249            (ii) MOLECULE TYPE: cDNA
250
251            (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
252
253    GAGCGCCGGC GCAACACCAT CGCCCCCAAC TGCGCGCTGC CGCCTGTGGC CCCCAACTGC     60
254    CTGGAGCTGC GGCGCCTCTG CTTCTCCGAC CCGCTTTGCA GATCACGCCT GGTGGATTTC    120
255    CAGACCCACT GCCATCCCAT GGACATCCTA GGAACTTGTG CAACAGAGCA GTCCAGATGT    180
256    CTACGAGCAT ACCTGGGGCT GATTGGGACT GCCATGACCC CCAACTTTGT CAGCAATGTC    240
257    AACACCAGTG TTGCCTTAAG CTGCACCTGC CGAGGCAGTG GCAACCTGCA GGAGGAGTGT    300
258    GAAATGCTGG AAGGGTTCTT CTCCCACAAC CCCTGCCTCA CGGAGGCCAT TGCAGCTAAG    360
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION   *US/08/977,862*

INPUT SET: S22663.raw

Line	Error		Original Text
27	Wrong application Serial Number		(A) APPLICATION NUMBER:To be assigned